AMENDMENTS TO THE CLAIMS:

1. - 4. (Canceled)

5. (Withdrawn) A computer-readable medium carrying microsatellite polymorphic marker distribution map and one or more sequences of instructions from a user of a computer system for analyzing said markers over a desired human genomic region, wherein the distribution map comprises information regarding the position of microsatellite polymorphic markers over one or more regions of the human genome, said markers being positioned at intervals of from about 50 Kb to 150 Kb, wherein execution of one or more sequences of instructions by one or more processors causes the one or more processor to perform a method, comprising:

receiving a query inputted by the user and receiving instructions as to a microsatellite markers or a human genomic region to include in analysis;

accessing distribution map information stored on the medium;

displaying a map showing the position of markers on a human genomic region, wherein the map provides at least the selected markers or markers within the selected region.

6. (Withdrawn) The computer-readable medium of claim 5, wherein the medium additionally carries sequence information for the markers.

7. (Withdrawn) The computer-readable medium of claim 6, wherein the sequence information comprises nucleotide sequences of SEQ ID NOS: 1-27088.

8. (Withdrawn) An isolated polynucleotide useful as a primer, the polynucleotide being about 15 to 100 nucleotides in length and containing a nucleotide sequence extending in 3'-direction from the 5'-terminus of a sequence of one of SEQ ID NOS: 1- 27088 or a nucleotide sequence complementary to a sequence extending in 5'-direction from the 3'-terminus of a sequence of one of SEQ ID NOS: 1-27088.

9. (Withdrawn) A method of assessing susceptibility of a human subject to psoriasis vulgaris, the method comprising:

analyzing a region of about 111 kb extending from C1_2_6 to C2_4_4 for the presence a marker that is associated with psoriasis vulgaris, wherein the marker is allele 303, allele 357, allele 255, allele 259, or allele 223;

wherein detection of the marker is indicative of susceptibility of the subject to psoriasis vulgaris.

10. (Withdrawn) The method of 9, wherein the marker is allele 303.

11. (Withdrawn) The method of claim 9, wherein the subject is heterozygous and is identified as a carrier for psoriasis vulgaris.

12. (Withdrawn) The method of claim 9, wherein the subject is homozygous, and is susceptible to onset or has psorasis vulgaris.

13. **(Currently Amended)** A gene mapping method, comprising:

selecting a combination of DNA sequences comprising SEQ ID Nos. 1-27088;

collecting DNA samples from affected subjects and control subjects;

performing polymerase chain reactions (PCR) using forward primers having a length of 15 to 100 nucleotides and having the same nucleotide sequence as the sequence extending in the 3'-direction from the 5'-terminus of each of the DNA sequences of **said combination** ~~**SEQ ID Nos: 1 to 27088 and**~~ reverse primers having a length of 15 to 100 nucleotides and having a nucleotide sequence complementary to the sequence extending in 5'-direction from the 3'-terminus of each of the DNA sequences of **said combination** ~~**SEQ ID Nos: 1 to 27088**~~ to produce DNA sequence fragments; wherein each of the fragments includes a microsatellite genetic polymorphism marker; and

statistically comparing the DNA sequence fragments of the affected subjects with the DNA sequence fragments of the control subjects to identify an existing region of a pathogenic gene or a gene relating to human phenotypes associated with a genetic factor.

14. (Previously Presented) The method according to claim 13, further comprising the step of mixing the DNA samples obtained from the affected subjects and control subjects to provide pooled DNA samples before performing the polymerase chain reaction.

15. (Previously Presented) The method according to claim 13, wherein the DNA sequence fragments produced by PCR comprise all or a part of the DNA sequences of SEQ ID Nos: 1 to 27088.

16. (Previously Presented) The method according to claim 13, wherein said comparing is carried out using a DNA chip and a mass spectrometer.

17. (Previously Presented) A gene mapping method according to claim 13, further comprising:

performing a second screening of DNA sequences comprising the microsatellite genetic polymorphism markers found positive through the method of claim 13 using DNA samples obtained from different affected subjects and the control subjects.

18. (Previously Presented) A gene mapping method according to claim 13, further comprising:

performing a genetic analysis on each group of the DNA sequences comprising the microsatellite genetic polymorphism markers found positive through the method of claim 13 using DNA samples obtained from a descent group having a pathogenic gene of affected subjects or a gene relating to human phenotypes with genetic factors; and

identifying a region of the DNA sequence including the microsatellite genetic polymorphism markers that are found true-positive.

19. (Previously Presented) A gene mapping method comprising analyzing an existing candidate DNA segment based on single nucleotide polymorphisms, wherein said candidate DNA segment includes a pathogenic gene or a gene relating to human phenotypes with genetic factors and wherein the candidate DNA segment was identified by the method according to claims 13, 14, 17, or 18.